Attachment

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 19, 2006, 08:51:36 ; Search time 298 Seconds
(without alignments)
1229.215 Million cell updates/sec

Title: US-10-469-221-2
Perfect score: 2106
Sequence: 1 SQGQSPPVPFPAPAPPPQPP.....PLLLKRRKKARALEAAALAH 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2106	100.0	400	1	MAPK2_HUMAN	P49137 homo sapien
2	2106	100.0	400	2	Q5SY41_HUMAN	Q5sy41 homo sapien
3	1931	91.7	386	1	MAPK2_MOUSE	P49138 mus musculu
4	1931	91.7	386	2	Q3U2P8_MOUSE	Q3u2p8 mus musculu
5	1930	91.6	386	2	Q80ZF4_RAT	Q80zf4 rattus norv
6	1882	89.4	370	2	Q5SY30_HUMAN	Q5sy30 homo sapien
7	1709	81.1	329	1	MAPK2_CRILO	P49136 cricetulus
8	1687	80.1	377	2	Q6IRB4_XENLA	Q6irb4 xenopus lae
9	1661.5	78.9	374	2	Q5XGX7_XENLA	Q5xgx7 xenopus lae
10	1645	78.1	382	2	Q7T2F2_BRARE	Q7t2f2 brachydanio
11	1536	72.9	330	1	MAPK2_RABIT	P49139 oryctolagus
12	1468	69.7	340	2	Q4SRA0_TETNG	Q4sra0 tetraodon n
13	1391	66.0	382	1	MAPK3_HUMAN	Q16644 homo sapien
14	1371	65.1	384	1	MAPK3_RAT	Q66h84 rattus norv
15	1370	65.1	384	1	MAPK3_BOVIN	Q3syz2 bos taurus
16	1361	64.6	384	1	MAPK3_MOUSE	Q3umw7 mus musculu
17	1344.5	63.8	418	2	Q4RXU6_TETNG	Q4rxu6 tetraodon n
18	1340	63.6	416	2	Q4SS24_TETNG	Q4ss24 tetraodon n
19	1266	60.1	353	2	Q2PQP1_GLOMR	Q2pqp1 glossina mo
20	1243.5	59.0	350	2	Q25108_HEMPU	Q25108 hemicentrot
21	1211.5	57.5	347	2	Q7PZG1_ANOGA	Q7pzg1 anopheles g
22	1201	57.0	359	1	MAPK2_DROME	P49071 drosophila
23	1060.5	50.4	391	2	Q61A12_CAEBR	Q61a12 caenorhabdi
24	1046	49.7	443	2	Q9TZ16_CAEEL	Q9tz16 caenorhabdi
25	1035	49.1	366	2	Q965G5_CAEEL	Q965g5 caenorhabdi
26	953	45.3	181	2	Q8R3U8_MOUSE	Q8r3u8 mus musculu
27	796.5	37.8	521	2	Q21360_CAEEL	Q21360 caenorhabdi
28	788	37.4	520	2	Q61ZD7_CAEBR	Q61zd7 caenorhabdi
29	740	35.1	495	2	Q6DEV6_XENTR	Q6dev6 xenopus tro
30	738	35.0	471	2	Q3UV25_MOUSE	Q3uv25 mus musculu
31	738	35.0	473	1	MAPK5_MOUSE	O54992 mus musculu
32	737.5	35.0	363	2	Q7JM88_CAEEL	Q7jm88 caenorhabdi
33	733	34.8	473	1	MAPK5_HUMAN	Q8iw41 homo sapien
34	730	34.7	471	2	Q6DHN7_BRARE	Q6dhn7 brachydanio
35	717	34.0	459	2	Q4RPT6_TETNG	Q4rpt6 tetraodon n
36	714.5	33.9	346	2	Q65ZB7_CAEEL	Q65zb7 caenorhabdi
37	655.5	31.1	238	2	Q65ZB6_CAEEL	Q65zb6 caenorhabdi
38	613	29.1	201	2	Q8T9D6_DROME	Q8t9d6 drosophila
39	566.5	26.9	249	2	Q8QGH1_CHICK	Q8qgh1 gallus gall
40	564	26.8	336	2	Q8I117_CAEEL	Q8i117 caenorhabdi
41	560.5	26.6	369	2	Q4KLJ9_RAT	Q4klj9 rattus norv
42	543.5	25.8	508	1	CDPK2_PLAF7	Q8icr0 plasmodium
43	543.5	25.8	512	1	CDPK2_PLAFK	O15865 plasmodium
44	540	25.6	578	2	Q5SVM5_HUMAN	Q5svm5 homo sapien
45	540	25.6	735	1	KS6A1_HUMAN	Q15418 homo sapien

ALIGNMENTS

RESULT 1
MAPK2_HUMAN
ID MAPK2_HUMAN STANDARD; PRT; 400 AA.
AC P49137; Q8IYD6;
DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1996, sequence version 1.
DT 07-MAR-2006, entry version 52.
DE MAP kinase-activated protein kinase 2 (EC 2.7.1.-) (MAPK-activated
DE protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2).
GN Name=MAPKAPK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=94235003; PubMed=8179591;
RA Zu Y.-L., Wu F., Gilchrist A., Ai Y., Labadia M.E., Huang C.K.;
RT "The primary structure of a human MAP kinase activated protein kinase
RT 2.";
RL Biochem. Biophys. Res. Commun. 200:1118-1124(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Skin, and Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 5-400.
RX MEDLINE=94107253; PubMed=8280084;
RA Stokoe D., Caudwell B., Cohen P.T.W., Cohen P.;
RT "The substrate specificity and structure of mitogen-activated protein
RT (MAP) kinase-activated protein kinase-2.";
RL Biochem. J. 296:843-849(1993).
RN [4]

```
RP   INTERACTION WITH PHC2.
RX   PubMed=15094067; DOI=10.1016/S0014-5793(04)00351-5;
RA   Yannoni Y.M., Gaestel M., Lin L.L.;
RT   "P66(ShcA) interacts with MAPKAP kinase 2 and regulates its
RT   activity.";
RL   FEBS Lett. 564:205-211(2004).
CC   -!- FUNCTION: Its physiological substrate seems to be the small heat
CC       shock protein (HSP27/HSP25). In vitro can phosphorylate glycogen
CC       synthase at Ser-7 and tyrosine hydroxylase (on Ser-19 and Ser-40).
CC       This kinase phosphorylates Ser in the peptide sequence, Hyd-X-R-
CC       X(2)-S, where Hyd is a large hydrophobic residue (By similarity).
CC   -!- ENZYME REGULATION: Seems to be activated by two distinct pathways:
CC       the first involves the stimulation of p42/p44 MAPK by growth
CC       factors, the second, triggered by stress and heat shock, depends
CC       on the activation of MPK2 and upstream MAPKK/MAPKKK.
CC   -!- SUBUNIT: Interacts with PHC2.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P49137-1; Sequence=Displayed;
CC         Note=Has a nuclear localization signal;
CC       Name=2;
CC         IsoId=P49137-2; Sequence=VSP_004910;
CC   -!- TISSUE SPECIFICITY: Expressed in all tissues examined.
CC   -!- PTM: Phosphorylated and activated by MAP kinase.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U12779; AAA20851.1; -; mRNA.
DR   EMBL; BC036060; AAH36060.2; -; mRNA.
DR   EMBL; BC052584; AAH52584.1; -; mRNA.
DR   EMBL; X75346; CAA53094.1; -; mRNA.
DR   PIR; JC2204; JC2204.
DR   PIR; S39793; S39793.
DR   PDB; 1KWP; X-ray; A/B=1-400.
DR   PDB; 1NXK; X-ray; A/B/C/D=1-400.
DR   PDB; 1NY3; X-ray; A=1-400.
DR   Ensembl; ENSG00000162889; Homo sapiens.
DR   HGNC; HGNC:6887; MAPKAPK2.
DR   MIM; 602006; gene.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0004871; F:signal transducer activity; TAS.
DR   GO; GO:0000165; P:MAPKKK cascade; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   3D-structure; Alternative splicing; ATP-binding; Kinase;
KW   Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;
KW   Transferase.
FT   CHAIN         1    400       MAP kinase-activated protein kinase 2.
FT                                /FTId=PRO_0000086288.
FT   DOMAIN       64    325       Protein kinase.
FT   NP_BIND      70     78       ATP (By similarity).
FT   COMPBIAS     10     40       Pro-rich.
FT   COMPBIAS     35     40       Poly-Pro.
FT   ACT_SITE    186    186       Proton acceptor.
FT   BINDING      93     93       ATP (By similarity).
FT   MOD_RES     328    328       Phosphoserine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     334    334       Phosphothreonine (by MAPK) (By
FT                                similarity).
FT               354    400       EEMTSALATMRVDYEQIKIKKIEDASNPLLLKRRKKARALE
FT                                AAALAH -> GCLHDKNSDQATWLTRL (in isoform
FT                                2).
FT                                /FTId=VSP_004910.
FT   CONFLICT    116    116       H -> D (in Ref. 3).
FT   CONFLICT    247    248       WS -> LV (in Ref. 3).
FT   HELIX        45     47
FT   STRAND       48     50
FT   STRAND       55     55
FT   STRAND       57     57
FT   HELIX        59     61
FT   TURN         62     62
FT   STRAND       63     73
FT   TURN         74     75
FT   STRAND       76     83
FT   TURN         84     86
FT   STRAND       89     96
FT   STRAND       98     98
FT   HELIX        99    111
FT   TURN        112    113
FT   STRAND      114    114
FT   TURN        115    116
FT   STRAND      117    117
FT   STRAND      120    128
FT   TURN        129    130
FT   STRAND      131    139
FT   STRAND      143    145
FT   HELIX       146    151
FT   STRAND      159    159
FT   HELIX       160    179
FT   TURN        180    181
FT   STRAND      182    183
FT   HELIX       189    191
FT   STRAND      192    198
FT   TURN        199    200
FT   STRAND      203    205
FT   TURN        209    210
FT   STRAND      212    213
FT   TURN        228    229
FT   HELIX       232    234
FT   STRAND      235    235
FT   STRAND      240    242
FT   HELIX       243    258
FT   STRAND      259    260
FT   STRAND      262    262
FT   TURN        267    268
FT   STRAND      270    271
FT   STRAND      274    274
FT   HELIX       275    281
FT   TURN        282    282
FT   TURN        288    293
FT   STRAND      294    294
FT   HELIX       296    303
FT   TURN        304    305
FT   STRAND      306    306
FT   STRAND      308    309
FT   HELIX       310    312
FT   STRAND      313    313
FT   HELIX       316    321
FT   STRAND      322    322
FT   HELIX       323    326
FT   TURN        327    329
FT   STRAND      330    331
FT   STRAND      335    335
FT   STRAND      337    337
FT   HELIX       338    344
SQ   SEQUENCE   400 AA;  45568 MW;  E4EFFF11CCF288DC CRC64;
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Query Match 100.0%; Score 2106; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 7.1e-115;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SQGQSPPVPFPAPAPPPQPPTPALPHPPAQPPPPPPQQFPQFHVKSGLQIKKNAIIDDYK 60
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```
              5 SQGQSPPVPFPAPAPPPQPPTPALPHPPAQPPPPPPQQFPQFHVKSGLQIKKNAIIDDYK 64

Qy           61 VTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           65 VTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 124

Qy          121 ENLYAGRKCLLIVMECLDGGELFSRIQDRGDQAFTEREASEIMKSIGEAIQYLHSINIAH 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          125 ENLYAGRKCLLIVMECLDGGELFSRIQDRGDQAFTEREASEIMKSIGEAIQYLHSINIAH 184

Qy          181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 244

Qy          241 DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFPNPEWSEVSEEVKMLIRN 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          245 DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFPNPEWSEVSEEVKMLIRN 304

Qy          301 LLKTEPTQRMTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          305 LLKTEPTQRMTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 364

Qy          361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
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Db          365 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 400
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RESULT 2
Q5SY41_HUMAN
ID   Q5SY41_HUMAN   PRELIMINARY;   PRT;   400 AA.
AC   Q5SY41;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Mitogen-activated protein kinase-activated protein kinase 2.
GN   Name=MAPKAPK2; ORFNames=RP11-343H5.3-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Harrison E.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AL591846; CAI13544.1; -; Genomic_DNA.
DR   SMR; Q5SY41; 41-357.
DR   Ensembl; ENSG00000162889; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   400 AA;  45568 MW;  E4EFFF11CCF288DC CRC64;

  Query Match             100.0%;  Score 2106;  DB 2;  Length 400;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-115;
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  Matches  396;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 SQGQSPPVPFPAPAPPPQPPTPALPHPPAQPPPPPPQQFPQFHVKSGLQIKKNAIIDDYK 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           5 SQGQSPPVPFPAPAPPPQPPTPALPHPPAQPPPPPPQQFPQFHVKSGLQIKKNAIIDDYK 64

Qy          61 VTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          65 VTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 124

Qy         121 ENLYAGRKCLLIVMECLDGGELFSRIQDRGDQAFTEREASEIMKSIGEAIQYLHSINIAH 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         125 ENLYAGRKCLLIVMECLDGGELFSRIQDRGDQAFTEREASEIMKSIGEAIQYLHSINIAH 184

Qy         181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 244

Qy         241 DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFPNPEWSEVSEEVKMLIRN 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         245 DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFPNPEWSEVSEEVKMLIRN 304

Qy         301 LLKTEPTQRMTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         305 LLKTEPTQRMTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 364

Qy         361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
               |||||||||||||||||||||||||||||||||||
Db         365 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 400
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RESULT 3
MAPK2_MOUSE
ID   MAPK2_MOUSE    STANDARD;      PRT;   386 AA.
AC   P49138; Q6P561;
DT   01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
DT   04-JAN-2005, sequence version 2.
DT   07-FEB-2006, entry version 47.
DE   MAP kinase-activated protein kinase 2 (EC 2.7.1.-) (MAPK-activated
DE   protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2).
GN   Name=Mapkapk2; Synonyms=Rps6kc1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 2-386.
RC   TISSUE=Lung;
RX   MEDLINE=94085571; PubMed=8262198; DOI=10.1016/0014-5793(93)81628-D;
RA   Engel K., Plath K., Gaestel M.;
RT   "The MAP kinase-activated protein kinase 2 contains a proline-rich
RT   SH3-binding domain.";
RL   FEBS Lett. 336:143-147(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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Qy        481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
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Db        871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 930

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Db        931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 990

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Db        991 CTCACTGACTTTGGCTTTGCCAAGGAAACCACCAGCCACAACTCTTTGACCACTCCTTGT 1050

Qy        661 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 720
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Db       1051 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 1110

Qy        721 GACATGTGGTCCCTGGGTGTCATCATGTACATCCTGCTGTGTGGGTATCCCCCCTTCTAC 780
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Qy        841 GAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
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Qy        901 CTGCTGAAAACAGAGCCCACCCAGAGAATGACCATCACCGAGTTTATGAACCACCCTTGG 960
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Db       1291 CTGCTGAAAACAGAGCCCACCCAGAGAATGACCATCACCGAGTTTATGAACCACCCTTGG 1350

Qy        961 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAGCCGGGTCCTGAAGGAG 1020
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Qy       1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
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RESULT 7
HSU12779
LOCUS HSU12779 2258 bp mRNA linear PRI 16-AUG-1994
DEFINITION Human MAP kinase activated protein kinase 2 mRNA, complete cds.
ACCESSION U12779
VERSION U12779.1 GI:530089
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2258)
AUTHORS Zu,Y.L., Wu,F., Gilchrist,A., Ai,Y., Labadia,M.E. and Huang,C.K.
TITLE The primary structure of a human MAP kinase activated protein kinase 2
JOURNAL Biochem. Biophys. Res. Commun. 200 (2), 1118-1124 (1994)
PUBMED 8179591
REFERENCE 2 (bases 1 to 2258)
AUTHORS Huang,C.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-1994) Chi-Kuang Huang, Pathology, University of Connecticut Health Center, 263 Farmington Ave., Farmington, CT 06030, USA
FEATURES Location/Qualifiers
source 1. .2258
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/db_xref="taxon:9606"
/clone="324"
/cell_line="HL-60"
CDS 379. .1491
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/product="MAP kinase activated protein kinase 2"
/protein_id="AAA20851.1"
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REASEIMKSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFGFAKETTSHN
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TRIRMGQYEFPNPEWSEVSEEVKMLIRNLLKTEPTQRMTITEFMNHPWIMQSTKVPQT
PLHTSRVLKEDKERWEDVKGCLHDKNSDQATWLTRL"
ORIGIN

Query Match 88.0%; Score 1048.4; DB 5; Length 2258;
Best Local Similarity 99.9%; Pred. No. 3.9e-274;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TCCCAGGGCCAGAGCCCGCCGGTGCCGTTCCCCGCCCCGGCCCCGCCGCCGCAGCCCCCC 60
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Db        391 TCCCAGGGCCAGAGCCCGCCGGTGCCGTTCCCCGCCCCGGCCCCGCCGCCGCAGCCCCCC 450

Qy         61 ACCCCTGCCCTGCCGCACCCCCCGGCGCAGCCGCCGCCGCCGCCCCCGCAGCAGTTCCCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 ACCCCTGCCCTGCCGCACCCCCCGGCGCAGCCGCCGCCGCCGCCCCCGCAGCAGTTCCCG 510

Qy        121 CAGTTCCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 180
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Db        511 CAGTTCCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 570

Qy        181 GTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAGTTTTGCAGATCTTCAACAAG 240
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Qy        241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAGGCCCGCAGGGAG 300
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Qy        361 GAGAATCTGTACGCAGGGAGGAAGTGCCTGCTGATTGTCATGGAATGTTTGGACGGTGGA 420
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Qy        421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAAGCATCC 480
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Qy        481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
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Db        871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 930

Qy        541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
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Db        931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 990

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Qy        661 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 720
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Db       1051 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 1110

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Qy        781 TCCAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
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Qy        841 GAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
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Qy        901 CTGCTGAAAACAGAGCCCACCCAGAGAATGACCATCACCGAGTTTATGAACCACCCTTGG 960
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Db       1291 CTGCTGAAAACAGAGCCCACCCAGAGAATGACCATCACCGAGTTTATGAACCACCCTTGG 1350

Qy        961 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAGCCGGGTCCTGAAGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAGCCGGGTCCTGAAGGAG 1410

Qy       1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
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RESULT 8
DD182194
LOCUS       DD182194                1305 bp    DNA     linear   PAT 19-DEC-2005
DEFINITION  Methods and Compositions for Protein Expression and Purification.
ACCESSION   DD182194
VERSION     DD182194.1  GI:83957055
KEYWORDS    JP 2005514025-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1305)
  AUTHORS   Malakhova,O.A., Butt,T.R., Tran,H.T., Malakhov,M.P. and Weeks,S.D.
  TITLE     Methods and Compositions for Protein Expression and Purification
  JOURNAL   Patent: JP 2005514025-A 15 19-MAY-2005;
            Tauseef Butt,Stephen Weeks,Hiep Tran,Oxana Malakhova, Micheal
            Malakhov
COMMENT     OS   Artificial Sequence
            PN   JP 2005514025-A/15
            PD   19-MAY-2005
            PF   07-JAN-2003 JP 2003557532
            PR   07-JAN-2002 US    60/346449
            PI   oxana a malakhova,tauseef r butt,hiep t tran,micheal p  PI
            malakhov,
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            CC   Synthetic Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             82.5%;  Score 982;  DB 2;  Length 1305;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-256;
  Matches  982;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 GCAGTTCCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAA 179
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Qy        180 GGTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAGTTTTGCAGATCTTCAACAA 239
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Qy        360 CGAGAATCTGTACGCAGGGAGGAAGTGCCTGCTGATTGTCATGGAATGTTTGGACGGTGG 419
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Db        561 CGAGAATCTGTACGCAGGGAGGAAGTGCCTGCTGATTGTCATGGAATGTTTGGACGGTGG 620

Qy        420 AGAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAAGCATC 479
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Qy        480 CGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCA 539
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Qy        540 TCGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAA 599
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Qy        660 TTATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTG 719
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Qy        780 CTCCAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTA 839
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Db        981 CTCCAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTA 1040

Qy        840 TGAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAA 899
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Qy        900 TCTGCTGAAAACAGAGCCCACCCAGAGAATGACCATCACCGAGTTTATGAACCACCCTTG 959
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Qy        960 GATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAGCCGGGTCCTGAAGGA 1019
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Qy       1020 GGACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAGTGCCTTGGCCACAATGCG 1079
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Db       1221 GGACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAGTGCCTTGGCCACAATGCG 1280

Qy       1080 CGTTGACTACGAGCAGATCAAG 1101
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RESULT 9
AY335730
LOCUS       AY335730                1065 bp    mRNA    linear   SYN 08-JUN-2005
DEFINITION  Synthetic construct Homo sapiens mitogen-activated protein
            kinase-activated protein kinase 2 (MAPKAPK2) mRNA, partial cds.
ACCESSION   AY335730
VERSION     AY335730.1  GI:33304098
KEYWORDS    FLI_CDNA.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1065)
  AUTHORS   Park,J., Hu,Y., Murthy,T.V.S., Vannberg,F., Shen,B., Rolfs,A.,
            Hutti,J.E., Cantley,L.C., LaBaer,J., Harlow,E. and Brizuela,L.
  TITLE     Building a human kinase gene repository: Bioinformatics, molecular
            cloning, and functional validation
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 102 (23), 8114-8119 (2005)
  PUBMED    15928075
REFERENCE   2  (bases 1 to 1065)
  AUTHORS   Park,J., Rolfs,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D.,
            Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E.,
            LaBaer,J. and Brizuela,L.
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